

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:13:58 ; Search time 101.503 Seconds  
 (without alignments)  
 2360.331 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	2789	100.0	524	2 AAR70783	Aar70783 Prosaposi
2	2789	100.0	524	2 AAW85652	Aaw85652 Human pro
3	2789	100.0	524	3 AAY58716	Aay58716 Human pro
4	2789	100.0	524	6 ABU79099	Abu79099 Lip-TAA b
5	2789	100.0	524	6 ABU05200	Abu05200 Human exp
6	2789	100.0	524	6 ABU05207	Abu05207 Human exp
7	2789	100.0	524	6 ABU05203	Abu05203 Human exp
8	2789	100.0	524	6 ABU07340	Abu07340 Human exp
9	2789	100.0	524	6 ABU05216	Abu05216 Human exp
10	2789	100.0	524	6 ABU05202	Abu05202 Human exp
11	2789	100.0	524	6 ABU05214	Abu05214 Human exp
12	2789	100.0	524	6 ABU05215	Abu05215 Human exp
13	2789	100.0	524	6 ABU05199	Abu05199 Human exp
14	2789	100.0	524	6 ABU05212	Abu05212 Human exp
15	2789	100.0	524	6 ABU05213	Abu05213 Human exp
16	2789	100.0	524	6 ABU05205	Abu05205 Human exp

17	2789	100.0	524	7	ADF43340	Adf43340 Superanti
18	2789	100.0	524	7	ADJ69401	Adj69401 Human hea
19	2789	100.0	524	8	ADO08060	Ado08060 Human pol
20	2789	100.0	524	8	ADQ94328	Adq94328 Human Pre
21	2789	100.0	524	8	ABM81149	Abm81149 Tumour-as
22	2789	100.0	524	8	ADS87894	Ads87894 Human pro
23	2789	100.0	524	8	ADU48630	Adu48630 Human pro
24	2789	100.0	524	9	ADW80727	Adw80727 Human pro
25	2789	100.0	524	9	ADX06774	Adx06774 Cyclin-de
26	2789	100.0	524	9	ADY14302	Ady14302 PRO polyp
27	2789	100.0	524	9	AED74803	Aed74803 Human pla
28	2779	99.6	524	6	ABU05208	Abu05208 Human exp
29	2777.5	99.6	527	4	AAB31915	Aab31915 Amino aci
30	2777.5	99.6	527	5	ABP68602	Abp68602 Human pan
31	2777.5	99.6	527	6	ABU79100	Abu79100 Lip-TAA b
32	2777.5	99.6	527	6	ABU05204	Abu05204 Human exp
33	2777.5	99.6	527	6	ABU05210	Abu05210 Human exp
34	2777.5	99.6	527	7	ADF43341	Adf43341 Superanti
35	2772.5	99.4	523	4	AAB31916	Aab31916 Amino aci
36	2772.5	99.4	523	6	ABU05211	Abu05211 Human exp
37	2768	99.2	526	6	ABU05209	Abu05209 Human exp
38	2767.5	99.2	527	6	ABU05206	Abu05206 Human exp
39	2731	97.9	522	8	ADU24090	Adu24090 Human cys
40	2449.5	87.8	479	6	ABR39442	Abr39442 Human GEN
41	2024.5	72.6	385	6	ABR41750	Abr41750 Human DIT
42	1969	70.6	554	7	ADB85295	Adb85295 Rat tubul
43	1921	68.9	554	5	ABB57102	Abb57102 Mouse isc
44	1293.5	46.4	268	8	ADP29875	Adp29875 Human sec
45	1201	43.1	507	8	ADS87898	Ads87898 Human hyp

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:21:31 ; Search time 65.0662 Seconds  
 (without alignments)  
 704.913 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	2789	100.0	524	2	US-09-352-548-1			Sequence 1, Appli
2	2789	100.0	524	2	US-09-949-016-6272			Sequence 6272, Ap
3	2789	100.0	524	2	US-08-928-074-23			Sequence 23, Appli
4	2789	100.0	535	2	US-09-949-016-8603			Sequence 8603, Ap
5	2766.5	99.2	523	1	US-08-100-247-2			Sequence 2, Appli
6	2766.5	99.2	523	2	US-08-756-031-2			Sequence 2, Appli
7	2759.5	98.9	523	1	US-08-232-513A-3			Sequence 3, Appli
8	2757.5	98.9	523	1	US-08-483-146A-2			Sequence 2, Appli
9	2757.5	98.9	523	1	US-08-484-594A-2			Sequence 2, Appli
10	2757.5	98.9	523	2	US-09-076-258A-2			Sequence 2, Appli
11	431	15.5	81	2	US-09-352-548-2			Sequence 2, Appli
12	418.5	15.0	80	1	US-08-584-671-15			Sequence 15, Appli
13	418.5	15.0	80	2	US-09-027-376-15			Sequence 15, Appli
14	418.5	15.0	80	6	US-09-878-099-15			Sequence 15, Appli
15	415.5	14.9	80	2	US-09-094-192-15			Sequence 15, Appli
16	412	14.8	80	1	US-08-100-247-3			Sequence 3, Appli
17	412	14.8	80	1	US-08-483-146A-3			Sequence 3, Appli
18	412	14.8	80	1	US-08-232-513A-4			Sequence 4, Appli
19	412	14.8	80	1	US-08-484-594A-3			Sequence 3, Appli

20	412	14.8	80	2	US-09-076-258A-3	Sequence 3, Appli
21	412	14.8	80	2	US-08-756-031-3	Sequence 3, Appli
22	412	14.8	80	2	US-08-928-074-24	Sequence 24, Appli
23	350.5	12.6	381	1	US-09-193-877-2	Sequence 2, Appli
24	349.5	12.5	381	2	US-09-949-016-10057	Sequence 10057, A
25	327	11.7	61	1	US-08-584-671-13	Sequence 13, Appli
26	327	11.7	61	2	US-09-027-376-13	Sequence 13, Appli
27	327	11.7	61	2	US-09-094-192-13	Sequence 13, Appli
28	327	11.7	61	6	US-09-878-099-13	Sequence 13, Appli
29	327	11.7	69	2	US-09-268-070-2	Sequence 2, Appli
30	322	11.5	79	1	US-08-584-671-16	Sequence 16, Appli
31	322	11.5	79	2	US-09-027-376-16	Sequence 16, Appli
32	322	11.5	79	2	US-09-094-192-16	Sequence 16, Appli
33	322	11.5	79	6	US-09-878-099-16	Sequence 16, Appli
34	321	11.5	79	1	US-08-584-671-14	Sequence 14, Appli
35	321	11.5	79	2	US-09-027-376-14	Sequence 14, Appli
36	321	11.5	79	2	US-09-094-192-14	Sequence 14, Appli
37	321	11.5	79	6	US-09-878-099-14	Sequence 14, Appli
38	268.5	9.6	257	2	US-08-596-684F-7	Sequence 7, Appli
39	239.5	8.6	60	1	US-08-584-671-12	Sequence 12, Appli
40	239.5	8.6	60	2	US-09-027-376-12	Sequence 12, Appli
41	239.5	8.6	60	2	US-09-268-070-4	Sequence 4, Appli
42	239.5	8.6	60	2	US-09-094-192-12	Sequence 12, Appli
43	239.5	8.6	60	6	US-09-878-099-12	Sequence 12, Appli
44	238.5	8.6	68	2	US-09-268-070-1	Sequence 1, Appli
45	211	7.6	40	2	US-09-780-438C-1	Sequence 1, Appli
46	208	7.5	67	2	US-09-268-070-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:23:10 ; Search time 216.887 Seconds  
 (without alignments)  
 1119.127 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	2789	100.0	524	3	US-09-870-759-60 Sequence 60, Appl
2	2789	100.0	524	3	US-09-751-708A-60 Sequence 60, Appl
3	2789	100.0	524	4	US-10-267-502-386 Sequence 386, App
4	2789	100.0	524	4	US-10-408-765A-1207 Sequence 1207, Ap
5	2789	100.0	524	4	US-10-746-442-23 Sequence 23, Appl
6	2789	100.0	524	4	US-10-428-817A-56 Sequence 56, Appl
7	2789	100.0	524	5	US-10-801-517-1 Sequence 1, Appli
8	2789	100.0	524	5	US-10-473-127-1865 Sequence 1865, Ap
9	2789	100.0	524	5	US-10-473-127-1866 Sequence 1866, Ap
10	2789	100.0	524	5	US-10-473-127-1868 Sequence 1868, Ap
11	2789	100.0	524	5	US-10-473-127-1869 Sequence 1869, Ap
12	2789	100.0	524	5	US-10-473-127-1871 Sequence 1871, Ap
13	2789	100.0	524	5	US-10-473-127-1873 Sequence 1873, Ap
14	2789	100.0	524	5	US-10-473-127-1878 Sequence 1878, Ap
15	2789	100.0	524	5	US-10-473-127-1879 Sequence 1879, Ap
16	2789	100.0	524	5	US-10-473-127-1880 Sequence 1880, Ap
17	2789	100.0	524	5	US-10-473-127-1881 Sequence 1881, Ap
18	2789	100.0	524	5	US-10-473-127-1882 Sequence 1882, Ap
19	2789	100.0	524	5	US-10-473-127-2041 Sequence 2041, Ap
20	2789	100.0	524	5	US-10-821-234-1631 Sequence 1631, Ap

21	2789	100.0	524	6	US-11-036-867-23	Sequence 23, Appl
22	2779	99.6	524	5	US-10-473-127-1874	Sequence 1874, Ap
23	2777.5	99.6	527	3	US-09-870-759-61	Sequence 61, Appl
24	2777.5	99.6	527	3	US-09-751-708A-61	Sequence 61, Appl
25	2777.5	99.6	527	4	US-10-060-036-73	Sequence 73, Appl
26	2777.5	99.6	527	4	US-10-428-817A-57	Sequence 57, Appl
27	2777.5	99.6	527	5	US-10-473-127-1870	Sequence 1870, Ap
28	2777.5	99.6	527	5	US-10-473-127-1876	Sequence 1876, Ap
29	2772.5	99.4	523	5	US-10-473-127-1877	Sequence 1877, Ap
30	2768	99.2	526	5	US-10-473-127-1875	Sequence 1875, Ap
31	2767.5	99.2	527	5	US-10-473-127-1872	Sequence 1872, Ap
32	2757.5	98.9	523	3	US-09-767-007A-2	Sequence 2, Appli
33	2731	97.9	522	5	US-10-618-281-38	Sequence 38, Appl
34	2449.5	87.8	479	3	US-09-978-418-40	Sequence 40, Appl
35	2449.5	87.8	479	5	US-10-485-231-40	Sequence 40, Appl
36	1969	70.6	554	4	US-10-205-194-176	Sequence 176, App
37	1201	43.1	521	4	US-10-276-162-1	Sequence 1, Appli
38	1201	43.1	521	6	US-11-002-844-1	Sequence 1, Appli
39	1151.5	41.3	227	4	US-10-452-858C-11	Sequence 11, Appl
40	1139.5	40.9	531	3	US-09-833-245-903	Sequence 903, App
41	1139.5	40.9	531	6	US-11-264-096-903	Sequence 903, App
42	1125	40.3	210	5	US-10-473-127-1867	Sequence 1867, Ap
43	1093	39.2	209	4	US-10-043-487-340	Sequence 340, App
44	834.5	29.9	362	4	US-10-332-426-8	Sequence 8, Appli

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:24:17 ; Search time 43:3775 Seconds  
 (without alignments)  
 959.216 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAYEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB ID	
1	2777.5	99.6	527	7 US-11-450-360-27	Sequence 27, Appl
2	2772.5	99.4	523	7 US-11-450-360-28	Sequence 28, Appl
3	545	19.5	241	7 US-11-293-697-4529	Sequence 4529, Ap
4	426.5	15.3	85	7 US-11-450-360-24	Sequence 24, Appl
5	414.5	14.9	83	7 US-11-450-360-74	Sequence 74, Appl
6	350.5	12.6	381	7 US-11-450-360-25	Sequence 25, Appl
7	335	12.0	380	7 US-11-450-360-29	Sequence 29, Appl
8	322.5	11.6	379	7 US-11-450-360-26	Sequence 26, Appl
9	292.5	10.5	370	6 US-10-527-191-111	Sequence 111, App
10	213	7.6	213	7 US-11-056-355B-38055	Sequence 38055, A
11	212	7.6	213	7 US-11-056-355B-38404	Sequence 38404, A
12	212	7.6	224	7 US-11-056-355B-38403	Sequence 38403, A
13	203.5	7.3	217	6 US-10-953-349-1507	Sequence 1507, Ap
14	203.5	7.3	217	7 US-11-056-355B-35428	Sequence 35428, A
15	203.5	7.3	217	7 US-11-056-355B-77551	Sequence 77551, A
16	186.5	6.7	217	7 US-11-056-355B-5699	Sequence 5699, Ap
17	186.5	6.7	224	7 US-11-056-355B-5698	Sequence 5698, Ap
18	184.5	6.6	184	7 US-11-056-355B-5700	Sequence 5700, Ap

19	184.5	6.6	223	6	US-10-449-902-38871	Sequence 38871, A
20	178.5	6.4	226	6	US-10-449-902-45769	Sequence 45769, A
21	176.5	6.3	205	7	US-11-056-355B-51890	Sequence 51890, A
22	176.5	6.3	233	7	US-11-056-355B-51889	Sequence 51889, A
23	176.5	6.3	235	7	US-11-056-355B-51888	Sequence 51888, A
24	175.5	6.3	229	7	US-11-056-355B-12182	Sequence 12182, A
25	171.5	6.1	205	6	US-10-953-349-7666	Sequence 7666, Ap
26	171.5	6.1	205	7	US-11-056-355B-30348	Sequence 30348, A
27	171.5	6.1	205	7	US-11-056-355B-33938	Sequence 33938, A
28	171.5	6.1	205	7	US-11-056-355B-65080	Sequence 65080, A
29	171.5	6.1	233	7	US-11-056-355B-65079	Sequence 65079, A
30	171.5	6.1	235	7	US-11-056-355B-65078	Sequence 65078, A
31	171.5	6.1	242	6	US-10-953-349-7665	Sequence 7665, Ap
32	171.5	6.1	242	7	US-11-056-355B-30347	Sequence 30347, A
33	171.5	6.1	242	7	US-11-056-355B-33937	Sequence 33937, A
34	171.5	6.1	278	6	US-10-953-349-7664	Sequence 7664, Ap
35	171.5	6.1	278	7	US-11-056-355B-30346	Sequence 30346, A
36	171.5	6.1	278	7	US-11-056-355B-33936	Sequence 33936, A
37	171.5	6.1	298	7	US-11-056-355B-28197	Sequence 28197, A
38	171.5	6.1	298	7	US-11-056-355B-31787	Sequence 31787, A
39	171.5	6.1	298	7	US-11-056-355B-47637	Sequence 47637, A
40	171.5	6.1	298	7	US-11-056-355B-97531	Sequence 97531, A
41	171.5	6.1	298	7	US-11-056-355B-108770	Sequence 108770,
42	171.5	6.1	486	7	US-11-056-355B-97530	Sequence 97530, A
43	171.5	6.1	486	7	US-11-056-355B-108769	Sequence 108769,
44	171.5	6.1	506	7	US-11-056-355B-28196	Sequence 28196, A
45	171.5	6.1	506	7	US-11-056-355B-31786	Sequence 31786, A

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:40 ; Search time 45.1126 Seconds  
 (without alignments)  
 1117.595 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
-----						
1	2777.5	99.6	527	1	SAHUP	saposin precursor
2	1996	71.6	554	1	A28716	saposin precursor
3	1937.5	69.5	557	1	JH0604	saposin precursor
4	511	18.3	965	2	T00207	P109 protein - sil
5	389	13.9	79	2	A49475	cerebroside sulfat
6	379	13.6	376	2	S02766	pulmonary surfacta
7	348.5	12.5	381	1	LNHUB	pulmonary surfacta
8	343	12.3	80	2	S21770	saposin-C - bovine
9	310	11.1	363	2	A29072	pulmonary surfacta
10	301.5	10.8	369	2	I46531	surfactant protein
11	261	9.4	81	2	A32026	glucosylceramide b
12	256.5	9.2	370	1	LNRBB	pulmonary surfacta
13	213	7.6	213	2	T46069	hypothetical prote
14	203.5	7.3	217	2	T48201	hypothetical prote
15	176.5	6.3	402	2	T15677	hypothetical prote
16	173.5	6.2	513	2	T09739	aspartic endopepti
17	171.5	6.1	506	2	F86253	hypothetical prote
18	165.5	5.9	506	2	T07915	probable aspartic
19	161.5	5.8	513	2	T11686	aspartic proteinas
20	161	5.8	428	2	S47096	cynarase (EC 3.4.2
21	161	5.8	474	2	T12049	cyprosin (EC 3.4.2
22	158.5	5.7	508	2	S19697	aspartic proteinas

23	156	5.6	314	2	T15674	hypothetical prote
24	155.5	5.6	292	2	T14446	aspartic proteinas
25	155.5	5.6	322	2	S41400	aspartic proteinas
26	154	5.5	496	2	JS0732	aspartic proteinas
27	153.5	5.5	509	2	JC7272	aspartic proteinas
28	145.5	5.2	205	2	B89567	protein T08A9.7 {i
29	143.5	5.1	1175	2	S52417	E-selectin ligand-
30	142.5	5.1	509	2	S49349	cyprosin (EC 3.4.2
31	142.5	5.1	509	2	S66516	oryzasin (EC 3.4.2
32	142.5	5.1	1948	2	S00485	gene 11-1 protein
33	141	5.1	508	2	D85056	probable aspartic
34	134	4.8	1927	2	G64585	cag pathogenicity
35	132.5	4.8	433	2	E96649	hypothetical prote
36	127.5	4.6	280	2	PC4080	aspartic proteinas
37	127.5	4.6	1142	2	A45031	cysteine-rich fibr
38	126.5	4.5	195	2	T15676	hypothetical prote
39	126.5	4.5	1819	2	A71928	cag island protein
40	126	4.5	506	2	S71591	aspartic proteinas
41	123.5	4.4	370	2	E96502	hypothetical prote
42	119	4.3	661	2	S67177	hypothetical prote
43	116.5	4.2	652	2	F85017	probable CHP-rich
44	116.5	4.2	707	2	T26218	hypothetical prote
45	116	4.2	975	2	I59422	rsec8 - rat (fragm

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:37 ; Search time 153.556 Seconds  
 (without alignments)  
 3156.550 Million cell updates/sec

Title: US-10-801-517-1  
 Perfect score: 2789  
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAYEHCKRHVWN 524

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2789	100.0	524	1	SAP_HUMAN	P07602 h proactiva
2	2789	100.0	524	2	Q5JQ36_HUMAN	Q5jq36 homo sapien
3	2785	99.9	524	2	Q53FJ5_HUMAN	Q53fj5 homo sapien
4	2783	99.8	559	2	Q5JQ37_HUMAN	Q5jq37 homo sapien
5	2777.5	99.6	530	2	Q59EN5_HUMAN	Q59en5 homo sapien
6	2776.5	99.6	527	2	Q5NVD5_PONPY	Q5nvd5 pongo pygma
7	2770	99.3	526	2	Q5R4U7_PONPY	Q5r4u7 pongo pygma
8	2451.5	87.9	497	2	Q4R590_MACFA	Q4r590 m brain cdn
9	2425.5	87.0	525	1	SAP_BOVIN	P26779 b proactiva
10	2374.5	85.1	452	2	Q5R406_PONPY	Q5r406 pongo pygma
11	1996	71.6	554	1	SAP_RAT	P10960 rattus norv
12	1982.5	71.1	553	2	Q6P7A4_RAT	Q6p7a4 rattus norv
13	1955	70.1	554	2	Q3TKB2_MOUSE	Q3tcb2 mus musculu
14	1953	70.0	554	2	Q3U897_MOUSE	Q3u897 mus musculu
15	1952	70.0	554	2	Q3TKK3_MOUSE	Q3tck3 mus musculu
16	1950	69.9	554	2	Q8BFQ1_MOUSE	Q8bfq1 m 2 days ne
17	1948	69.8	554	2	Q3TWE9_MOUSE	Q3twe9 mus musculu
18	1947	69.8	554	2	Q3TID4_MOUSE	Q3tid4 mus musculu
19	1947	69.8	554	2	Q3TWL8_MOUSE	Q3twl8 mus musculu
20	1946	69.8	554	2	Q3U825_MOUSE	Q3u825 mus musculu
21	1946	69.8	554	2	Q3U8C4_MOUSE	Q3u8c4 mus musculu
22	1945	69.7	554	2	Q3TIT5_MOUSE	Q3tit5 mus musculu
23	1944	69.7	554	2	Q3U5W2_MOUSE	Q3u5w2 mus musculu
24	1941	69.6	554	2	Q3TWF9_MOUSE	Q3twf9 mus musculu

25	1940	69.6	554	2	Q3TXP9_MOUSE	Q3txp9 mus musculu
26	1938.5	69.5	553	2	Q3TXJ0_MOUSE	Q3txj0 m osteoclas
27	1938.5	69.5	557	1	SAP_MOUSE	Q61207 mus musculu
28	1938.5	69.5	557	2	Q3UFE8_MOUSE	Q3ufe8 mus musculu
29	1900	68.1	551	2	Q3UE29_MOUSE	Q3ue29 mus musculu
30	1899.5	68.1	545	2	Q3UAS4_MOUSE	Q3uas4 m bone marr
31	1887	67.7	527	2	Q3TWM9_MOUSE	Q3twm9 mus musculu
32	1679.5	60.2	518	1	SAP_CHICK	O13035 gallus gall
33	1442	51.7	512	2	Q7SY70_XENLA	Q7sy70 xenopus lae
34	1429	51.2	518	2	Q642S6_XENLA	Q642s6 xenopus lae
35	1416	50.8	550	2	Q4RQ38_TETNG	Q4rq38 tetraodon n
36	1414	50.7	520	2	Q8UVZ4_BRARE	Q8uvz4 brachydanio
37	1412	50.6	520	2	Q6PH48_BRARE	Q6ph48 brachydanio
38	1411	50.6	520	2	Q6P3G7_BRARE	Q6p3g7 brachydanio
39	1343	48.2	522	2	Q9DG82_BRARE	Q9dg82 brachydanio
40	1201	43.1	543	2	Q6NUJ1_HUMAN	Q6nuj1 homo sapien
41	1153	41.3	240	2	Q5BJH1_HUMAN	Q5bjh1 homo sapien
42	1099.5	39.4	525	2	Q8C1C1_MOUSE	Q8c1c1 mus musculu
43	803	28.8	245	2	Q5ZL62_CHICK	Q5zl62 gallus gall
44	786	28.2	449	2	Q8BJV5_MOUSE	Q8bjv5 mus musculu
45	772	27.7	402	2	Q8C1N0_MOUSE	Q8c1n0 mus musculu

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:13:58 ; Search time 15.4967 Seconds  
 (without alignments)  
 2360.331 Million cell updates/sec

Title: US-10-801-517-2  
 Perfect score: 412  
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPGVCSMLHLCG 80

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : A\_Geneseq\_8:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*  
 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	412	100.0	80	2	AAR70784	Aar70784 Saposin-C
2	412	100.0	80	2	AAW85653	Aaw85653 Human sap
3	412	100.0	80	4	AAU05697	Aau05697 Human Sap
4	412	100.0	80	7	ABU62252	Abu62252 Sphingoli
5	412	100.0	80	8	ADQ94329	Adq94329 Human Pre
6	412	100.0	80	8	ADU48631	Adu48631 Human Sap
7	412	100.0	80	9	ADW80728	Adw80728 Human sap
8	412	100.0	80	9	ADZ88479	Adz88479 Human sap
9	412	100.0	210	6	ABU05201	Abu05201 Human exp
10	412	100.0	385	6	ABR41750	Abr41750 Human DIT
11	412	100.0	479	6	ABR39442	Abr39442 Human GEN
12	412	100.0	522	8	ADU24090	Adu24090 Human cys
13	412	100.0	523	4	AAB31916	Aab31916 Amino aci
14	412	100.0	523	6	ABU05211	Abu05211 Human exp
15	412	100.0	524	2	AAR70783	Aar70783 Prosaposi
16	412	100.0	524	2	AAW85652	Aaw85652 Human pro

17	412	100.0	524	3	AAY58716	Aay58716 Human pro
18	412	100.0	524	6	ABU79099	Abu79099 Lip-TAA b
19	412	100.0	524	6	ABU05200	Abu05200 Human exp
20	412	100.0	524	6	ABU05207	Abu05207 Human exp
21	412	100.0	524	6	ABU05203	Abu05203 Human exp
22	412	100.0	524	6	ABU07340	Abu07340 Human exp
23	412	100.0	524	6	ABU05216	Abu05216 Human exp
24	412	100.0	524	6	ABU05202	Abu05202 Human exp
25	412	100.0	524	6	ABU05208	Abu05208 Human exp
26	412	100.0	524	6	ABU05214	Abu05214 Human exp
27	412	100.0	524	6	ABU05215	Abu05215 Human exp
28	412	100.0	524	6	ABU05199	Abu05199 Human exp
29	412	100.0	524	6	ABU05212	Abu05212 Human exp
30	412	100.0	524	6	ABU05213	Abu05213 Human exp
31	412	100.0	524	6	ABU05205	Abu05205 Human exp
32	412	100.0	524	7	ADF43340	Adf43340 Superanti
33	412	100.0	524	7	ADJ69401	Adj69401 Human hea
34	412	100.0	524	8	ADO08060	Ado08060 Human pol
35	412	100.0	524	8	ADQ94328	Adq94328 Human Pre
36	412	100.0	524	8	ABM81149	Abm81149 Tumour-as
37	412	100.0	524	8	ADS87894	Ads87894 Human pro
38	412	100.0	524	8	ADU48630	Adu48630 Human pro
39	412	100.0	524	9	ADW80727	Adw80727 Human pro
40	412	100.0	524	9	ADX06774	Adx06774 Cyclin-de
41	412	100.0	524	9	ADY14302	Ady14302 PRO polyp
42	412	100.0	524	9	AED74803	Aed74803 Human pla
43	412	100.0	526	6	ABU05209	Abu05209 Human exp
44	412	100.0	527	4	AAB31915	Aab31915 Amino aci
45	412	100.0	527	5	ABP68602	Abp68602 Human pan
46	412	100.0	527	6	ABU79100	Abu79100 Lip-TAA b
47	412	100.0	527	6	ABU05206	Abu05206 Human exp
48	412	100.0	527	6	ABU05204	Abu05204 Human exp
49	412	100.0	527	6	ABU05210	Abu05210 Human exp
50	412	100.0	527	7	ADF43341	Adf43341 Superanti
51	412	100.0	592	4	AAU05698	Aau05698 Human glu
52	355	86.2	227	8	ADO57419	Ado57419 Hairless
53	283.5	68.8	268	8	ADP29875	Adp29875 Human sec

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:21:31 ; Search time 9.93377 Seconds  
 (without alignments)  
 704.913 Million cell updates/sec

Title: US-10-801-517-2  
 Perfect score: 412  
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPLEVCSMLHLC 80

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*

1:	/EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:	/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:	/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:	/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:	/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:	/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:	/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	412	100.0	80	1	US-08-100-247-3	Sequence 3, Appli
2	412	100.0	80	1	US-08-483-146A-3	Sequence 3, Appli
3	412	100.0	80	1	US-08-232-513A-4	Sequence 4, Appli
4	412	100.0	80	1	US-08-484-594A-3	Sequence 3, Appli
5	412	100.0	80	2	US-09-076-258A-3	Sequence 3, Appli
6	412	100.0	80	2	US-08-756-031-3	Sequence 3, Appli
7	412	100.0	80	2	US-08-928-074-24	Sequence 24, Appli
8	412	100.0	523	1	US-08-100-247-2	Sequence 2, Appli
9	412	100.0	523	1	US-08-483-146A-2	Sequence 2, Appli
10	412	100.0	523	1	US-08-232-513A-3	Sequence 3, Appli
11	412	100.0	523	1	US-08-484-594A-2	Sequence 2, Appli
12	412	100.0	523	2	US-09-076-258A-2	Sequence 2, Appli
13	412	100.0	523	2	US-08-756-031-2	Sequence 2, Appli
14	412	100.0	524	2	US-09-352-548-1	Sequence 1, Appli
15	412	100.0	524	2	US-09-949-016-6272	Sequence 6272, Ap
16	412	100.0	524	2	US-08-928-074-23	Sequence 23, Appli
17	412	100.0	535	2	US-09-949-016-8603	Sequence 8603, Ap
18	211	51.2	40	2	US-09-780-438C-1	Sequence 1, Appli
19	201	48.8	38	2	US-09-780-438C-2	Sequence 2, Appli

20	111	26.9	22	1	US-08-100-247-1	Sequence 1, Appli
21	111	26.9	22	1	US-08-483-146A-1	Sequence 1, Appli
22	111	26.9	22	1	US-08-232-513A-1	Sequence 1, Appli
23	111	26.9	22	1	US-08-484-594A-1	Sequence 1, Appli
24	111	26.9	22	2	US-09-231-159-1	Sequence 1, Appli
25	111	26.9	22	2	US-08-611-307-1	Sequence 1, Appli
26	111	26.9	22	2	US-09-148-030-1	Sequence 1, Appli
27	111	26.9	22	2	US-09-076-258A-1	Sequence 1, Appli
28	111	26.9	22	2	US-08-756-031-1	Sequence 1, Appli
29	111	26.9	22	2	US-08-928-074-1	Sequence 1, Appli
30	106	25.7	22	2	US-09-231-159-8	Sequence 8, Appli
31	106	25.7	22	2	US-08-611-307-8	Sequence 8, Appli
32	106	25.7	22	2	US-08-928-074-8	Sequence 8, Appli
33	101	24.5	38	2	US-09-780-438C-3	Sequence 3, Appli
34	101	24.5	38	2	US-09-780-438C-5	Sequence 5, Appli
35	101	24.5	38	2	US-09-780-438C-6	Sequence 6, Appli
36	101	24.5	39	2	US-09-780-438C-4	Sequence 4, Appli
37	96	23.3	22	1	US-08-483-146A-9	Sequence 9, Appli
38	96	23.3	22	1	US-08-232-513A-18	Sequence 18, Appli
39	96	23.3	22	1	US-08-484-594A-9	Sequence 9, Appli
40	96	23.3	22	2	US-09-231-159-7	Sequence 7, Appli
41	96	23.3	22	2	US-08-611-307-7	Sequence 7, Appli
42	96	23.3	22	2	US-09-076-258A-9	Sequence 9, Appli
43	96	23.3	22	2	US-08-928-074-7	Sequence 7, Appli
44	96	23.3	514	2	US-10-339-351-2	Sequence 2, Appli
45	92	22.3	79	2	US-08-596-684F-6	Sequence 6, Appli
46	92	22.3	79	2	US-09-515-356-1	Sequence 1, Appli
47	92	22.3	181	2	US-08-848-580-12	Sequence 12, Appli
48	92	22.3	181	2	US-08-488-123-12	Sequence 12, Appli
49	92	22.3	257	2	US-08-596-684F-7	Sequence 7, Appli
50	92	22.3	381	2	US-09-949-016-10057	Sequence 10057, A
51	91	22.1	79	2	US-09-788-308E-2	Sequence 2, Appli
52	91	22.1	381	1	US-09-193-877-2	Sequence 2, Appli
53	88	21.4	514	2	US-10-339-351-1	Sequence 1, Appli
54	88	21.4	514	2	US-10-339-351-3	Sequence 3, Appli
55	83	20.1	18	1	US-08-100-247-5	Sequence 5, Appli
56	83	20.1	18	1	US-08-483-146A-5	Sequence 5, Appli
57	83	20.1	18	1	US-08-232-513A-6	Sequence 6, Appli
58	83	20.1	18	1	US-08-484-594A-5	Sequence 5, Appli
59	83	20.1	18	2	US-09-231-159-20	Sequence 20, Appli
60	83	20.1	18	2	US-08-611-307-20	Sequence 20, Appli
61	83	20.1	18	2	US-09-148-030-2	Sequence 2, Appli
62	83	20.1	18	2	US-09-076-258A-5	Sequence 5, Appli
63	83	20.1	18	2	US-08-756-031-5	Sequence 5, Appli
64	83	20.1	18	2	US-08-928-074-20	Sequence 20, Appli
65	80.5	19.5	78	1	US-08-732-228-1	Sequence 1, Appli
66	75	18.2	15	2	US-09-148-030-10	Sequence 10, Appli

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:23:10 ; Search time 33.1126 Seconds  
 (without alignments)  
 1119.127 Million cell updates/sec

Title: US-10-801-517-2  
 Perfect score: 412  
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPERVCSMLHLCG 80

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	412	100.0	80	3	US-09-767-007A-3	Sequence 3, Appli
2	412	100.0	80	3	US-09-753-126-3	Sequence 3, Appli
3	412	100.0	80	4	US-10-330-697-3	Sequence 3, Appli
4	412	100.0	80	4	US-10-746-442-24	Sequence 24, Appli
5	412	100.0	80	5	US-10-801-517-2	Sequence 2, Appli
6	412	100.0	80	6	US-11-036-867-24	Sequence 24, Appli
7	412	100.0	210	5	US-10-473-127-1867	Sequence 1867, Appli
8	412	100.0	479	3	US-09-978-418-40	Sequence 40, Appli
9	412	100.0	479	5	US-10-485-231-40	Sequence 40, Appli
10	412	100.0	522	5	US-10-618-281-38	Sequence 38, Appli
11	412	100.0	523	3	US-09-767-007A-2	Sequence 2, Appli
12	412	100.0	523	5	US-10-473-127-1877	Sequence 1877, Appli
13	412	100.0	524	3	US-09-870-759-60	Sequence 60, Appli
14	412	100.0	524	3	US-09-751-708A-60	Sequence 60, Appli
15	412	100.0	524	4	US-10-267-502-386	Sequence 386, Appli
16	412	100.0	524	4	US-10-408-765A-1207	Sequence 1207, Appli
17	412	100.0	524	4	US-10-746-442-23	Sequence 23, Appli
18	412	100.0	524	4	US-10-428-817A-56	Sequence 56, Appli
19	412	100.0	524	5	US-10-801-517-1	Sequence 1, Appli
20	412	100.0	524	5	US-10-473-127-1865	Sequence 1865, Appli

21	412	100.0	524	5	US-10-473-127-1866	Sequence 1866, Ap
22	412	100.0	524	5	US-10-473-127-1868	Sequence 1868, Ap
23	412	100.0	524	5	US-10-473-127-1869	Sequence 1869, Ap
24	412	100.0	524	5	US-10-473-127-1871	Sequence 1871, Ap
25	412	100.0	524	5	US-10-473-127-1873	Sequence 1873, Ap
26	412	100.0	524	5	US-10-473-127-1874	Sequence 1874, Ap
27	412	100.0	524	5	US-10-473-127-1878	Sequence 1878, Ap
28	412	100.0	524	5	US-10-473-127-1879	Sequence 1879, Ap
29	412	100.0	524	5	US-10-473-127-1880	Sequence 1880, Ap
30	412	100.0	524	5	US-10-473-127-1881	Sequence 1881, Ap
31	412	100.0	524	5	US-10-473-127-1882	Sequence 1882, Ap
32	412	100.0	524	5	US-10-473-127-2041	Sequence 2041, Ap
33	412	100.0	524	5	US-10-821-234-1631	Sequence 1631, Ap
34	412	100.0	524	6	US-11-036-867-23	Sequence 23, Appl
35	412	100.0	526	5	US-10-473-127-1875	Sequence 1875, Ap
36	412	100.0	527	3	US-09-870-759-61	Sequence 61, Appl
37	412	100.0	527	3	US-09-751-708A-61	Sequence 61, Appl
38	412	100.0	527	4	US-10-060-036-73	Sequence 73, Appl
39	412	100.0	527	4	US-10-428-817A-57	Sequence 57, Appl
40	412	100.0	527	5	US-10-473-127-1870	Sequence 1870, Ap
41	412	100.0	527	5	US-10-473-127-1872	Sequence 1872, Ap
42	412	100.0	527	5	US-10-473-127-1876	Sequence 1876, Ap
43	412	100.0	592	3	US-09-753-126-4	Sequence 4, Appli
44	412	100.0	592	4	US-10-330-697-4	Sequence 4, Appli
45	355	86.2	227	4	US-10-452-858C-11	Sequence 11, Appl
46	257	62.4	209	4	US-10-043-487-340	Sequence 340, App

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:24:17 ; Search time 6.62252 Seconds  
 (without alignments)  
 959.216 Million cell updates/sec

Title: US-10-801-517-2

Perfect score: 412

Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPERVCSMLHLC 80

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	412	100.0	523	7	US-11-450-360-28	Sequence 28, Appl
2	412	100.0	527	7	US-11-450-360-27	Sequence 27, Appl
3	147.5	35.8	241	7	US-11-293-697-4529	Sequence 4529, Ap.
4	115	27.9	223	6	US-10-449-902-38871	Sequence 38871, A
5	106.5	25.8	135	6	US-10-953-349-1508	Sequence 1508, Ap
6	106.5	25.8	135	7	US-11-056-355B-35429	Sequence 35429, A
7	106.5	25.8	135	7	US-11-056-355B-77552	Sequence 77552, A
8	106.5	25.8	217	6	US-10-953-349-1507	Sequence 1507, Ap
9	106.5	25.8	217	7	US-11-056-355B-35428	Sequence 35428, A
10	106.5	25.8	217	7	US-11-056-355B-77551	Sequence 77551, A
11	106	25.7	213	7	US-11-056-355B-38055	Sequence 38055, A
12	106	25.7	213	7	US-11-056-355B-38404	Sequence 38404, A
13	106	25.7	224	6	US-10-953-349-16163	Sequence 16163, A
14	106	25.7	224	7	US-11-056-355B-38403	Sequence 38403, A
15	106	25.7	224	7	US-11-056-355B-55976	Sequence 55976, A
16	104	25.2	184	7	US-11-056-355B-5700	Sequence 5700, Ap
17	104	25.2	205	6	US-10-953-349-7666	Sequence 7666, Ap
18	104	25.2	205	7	US-11-056-355B-30348	Sequence 30348, A

19	104	25.2	205	7	US-11-056-355B-33938	Sequence 33938, A
20	104	25.2	217	7	US-11-056-355B-5699	Sequence 5699, Ap
21	104	25.2	224	7	US-11-174-307B-4380	Sequence 4380, Ap
22	104	25.2	224	7	US-11-056-355B-5698	Sequence 5698, Ap
23	104	25.2	242	6	US-10-953-349-7665	Sequence 7665, Ap
24	104	25.2	242	7	US-11-056-355B-30347	Sequence 30347, A
25	104	25.2	242	7	US-11-056-355B-33937	Sequence 33937, A
26	104	25.2	278	6	US-10-953-349-7664	Sequence 7664, Ap
27	104	25.2	278	7	US-11-056-355B-30346	Sequence 30346, A
28	104	25.2	278	7	US-11-056-355B-33936	Sequence 33936, A
29	104	25.2	298	7	US-11-056-355B-28197	Sequence 28197, A
30	104	25.2	298	7	US-11-056-355B-31787	Sequence 31787, A
31	104	25.2	298	7	US-11-056-355B-47637	Sequence 47637, A
32	104	25.2	298	7	US-11-056-355B-97531	Sequence 97531, A
33	104	25.2	298	7	US-11-056-355B-108770	Sequence 108770,
34	104	25.2	486	7	US-11-056-355B-97530	Sequence 97530, A
35	104	25.2	486	7	US-11-056-355B-108769	Sequence 108769,
36	104	25.2	506	7	US-11-056-355B-28196	Sequence 28196, A
37	104	25.2	506	7	US-11-056-355B-31786	Sequence 31786, A
38	104	25.2	506	7	US-11-056-355B-47636	Sequence 47636, A
39	104	25.2	522	7	US-11-056-355B-28195	Sequence 28195, A
40	104	25.2	522	7	US-11-056-355B-31785	Sequence 31785, A
41	104	25.2	522	7	US-11-056-355B-47635	Sequence 47635, A
42	103	25.0	229	7	US-11-056-355B-12182	Sequence 12182, A
43	103	25.0	298	7	US-11-056-355B-100544	Sequence 100544,
44	103	25.0	298	7	US-11-056-355B-111783	Sequence 111783,
45	103	25.0	513	7	US-11-056-355B-100543	Sequence 100543,
46	103	25.0	513	7	US-11-056-355B-111782	Sequence 111782,
47	103	25.0	521	7	US-11-056-355B-100542	Sequence 100542,
48	103	25.0	521	7	US-11-056-355B-111781	Sequence 111781,
49	100	24.3	205	7	US-11-056-355B-65080	Sequence 65080, A
50	100	24.3	233	7	US-11-056-355B-65079	Sequence 65079, A
51	100	24.3	235	7	US-11-056-355B-65078	Sequence 65078, A
52	100	24.3	237	7	US-11-056-355B-13179	Sequence 13179, A
53	100	24.3	293	7	US-11-056-355B-2204	Sequence 2204, Ap
54	100	24.3	294	7	US-11-056-355B-13178	Sequence 13178, A
55	100	24.3	294	7	US-11-056-355B-14163	Sequence 14163, A
56	100	24.3	504	7	US-11-056-355B-14162	Sequence 14162, A
57	100	24.3	516	7	US-11-056-355B-2203	Sequence 2203, Ap
58	99	24.0	205	7	US-11-056-355B-51890	Sequence 51890, A
59	99	24.0	233	7	US-11-056-355B-51889	Sequence 51889, A
60	99	24.0	235	7	US-11-056-355B-51888	Sequence 51888, A
61	98	23.8	226	6	US-10-449-902-45769	Sequence 45769, A
62	98	23.8	496	6	US-10-449-902-43086	Sequence 43086, A
63	97	23.5	241	6	US-10-953-349-28839	Sequence 28839, A
64	97	23.5	241	7	US-11-056-355B-68617	Sequence 68617, A
65	97	23.5	266	6	US-10-449-902-53649	Sequence 53649, A
66	97	23.5	273	6	US-10-953-349-28838	Sequence 28838, A
67	97	23.5	273	7	US-11-056-355B-68616	Sequence 68616, A
68	97	23.5	509	6	US-10-449-902-33141	Sequence 33141, A
69	97	23.5	509	6	US-10-449-902-43057	Sequence 43057, A
70	97	23.5	509	6	US-10-449-902-43119	Sequence 43119, A
71	97	23.5	509	6	US-10-449-902-44368	Sequence 44368, A
72	97	23.5	509	6	US-10-449-902-45701	Sequence 45701, A
73	97	23.5	509	6	US-10-449-902-56301	Sequence 56301, A
74	96	23.3	256	7	US-11-056-355B-8801	Sequence 8801, Ap
75	96	23.3	258	7	US-11-056-355B-16289	Sequence 16289, A
76	96	23.3	281	7	US-11-056-355B-8800	Sequence 8800, Ap
77	96	23.3	473	7	US-11-056-355B-16288	Sequence 16288, A
78	96	23.3	508	7	US-11-056-355B-16287	Sequence 16287, A
79	94.5	22.9	370	6	US-10-527-191-111	Sequence 111, App
80	92	22.3	380	7	US-11-450-360-29	Sequence 29, Appl
81	92	22.3	450	6	US-10-953-349-13719	Sequence 13719, A
82	92	22.3	451	6	US-10-953-349-13718	Sequence 13718, A
83	92	22.3	508	6	US-10-953-349-13717	Sequence 13717, A

84	91	22.1	295	6	US-10-953-349-8827	Sequence 8827, Ap
85	91	22.1	295	6	US-10-953-349-10645	Sequence 10645, A
86	91	22.1	295	7	US-11-056-355B-37269	Sequence 37269, A
87	91	22.1	295	7	US-11-056-355B-43886	Sequence 43886, A
88	91	22.1	295	7	US-11-056-355B-50072	Sequence 50072, A
89	91	22.1	381	7	US-11-450-360-25	Sequence 25, Appl
90	91	22.1	433	6	US-10-953-349-8826	Sequence 8826, Ap
91	91	22.1	433	6	US-10-953-349-10644	Sequence 10644, A
92	91	22.1	433	7	US-11-056-355B-37268	Sequence 37268, A
93	91	22.1	433	7	US-11-056-355B-43885	Sequence 43885, A
94	91	22.1	433	7	US-11-056-355B-50071	Sequence 50071, A
95	91	22.1	508	6	US-10-953-349-8825	Sequence 8825, Ap
96	91	22.1	508	6	US-10-953-349-10643	Sequence 10643, A
97	91	22.1	508	7	US-11-056-355B-37267	Sequence 37267, A
98	91	22.1	508	7	US-11-056-355B-43884	Sequence 43884, A
99	91	22.1	508	7	US-11-056-355B-50070	Sequence 50070, A
100	89.5	21.7	118	7	US-11-056-355B-12183	Sequence 12183, A
101	88	21.4	237	6	US-10-449-902-31627	Sequence 31627, A
102	88	21.4	495	6	US-10-449-902-44439	Sequence 44439, A
103	88	21.4	495	6	US-10-449-902-50431	Sequence 50431, A
104	88	21.4	495	6	US-10-449-902-53322	Sequence 53322, A
105	87	21.1	392	6	US-10-953-349-36927	Sequence 36927, A
106	87	21.1	503	6	US-10-953-349-36926	Sequence 36926, A
107	87	21.1	525	6	US-10-953-349-36925	Sequence 36925, A
108	86.5	21.0	106	7	US-11-056-355B-38056	Sequence 38056, A
109	86	20.9	233	7	US-11-056-355B-7597	Sequence 7597, Ap
110	86	20.9	448	7	US-11-056-355B-7596	Sequence 7596, Ap
111	85	20.6	413	6	US-10-449-902-50838	Sequence 50838, A
112	85	20.6	522	6	US-10-449-902-50452	Sequence 50452, A
113	80.5	19.5	78	7	US-11-368-086-64	Sequence 64, Appl
114	79.5	19.3	379	7	US-11-450-360-26	Sequence 26, Appl

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:40 ; Search time 6.88742 Seconds  
(without alignments)  
1117.595 Million cell updates/sec

Title: US-10-801-517-2

Perfect score: 412

Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPVELVCSMLHLC 80

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB	
1	412	100.0	527	1	SAHUP saposin precursor
2	343	83.3	80	2	S21770 saposin-C - bovine
3	261	63.3	81	2	A32026 glucosylceramide b
4	193	46.8	554	1	A28716 saposin precursor
5	168	40.8	557	1	JH0604 saposin precursor
6	158	38.3	965	2	T00207 P109 protein - sil
7	106.5	25.8	217	2	T48201 hypothetical prote
8	106	25.7	213	2	T46069 hypothetical prote
9	106	25.7	428	2	S47096 cynarase (EC 3.4.2)
10	106	25.7	474	2	T12049 cyprosin (EC 3.4.2)
11	104	25.2	506	2	F86253 hypothetical prote
12	103	25.0	292	2	T14446 aspartic proteinas
13	103	25.0	322	2	S41400 aspartic proteinas
14	103	25.0	433	2	E96649 hypothetical prote
15	102.5	24.9	376	2	S02766 pulmonary surfacta
16	102	24.8	506	2	T07915 probable aspartic
17	102	24.8	509	2	JC7272 aspartic proteinas
18	100	24.3	513	2	T11686 aspartic proteinas
19	99.5	24.2	103	2	D89567 protein T08A9.8 [i]
20	99.5	24.2	363	2	A29072 pulmonary surfacta
21	99	24.0	575	1	A40292 acyloxyacyl hydrol
22	98	23.8	496	2	JS0732 aspartic proteinas

23	97	23.5	508	2	S19697	aspartic proteinas
24	97	23.5	509	2	S66516	oryzasin (EC 3.4.2
25	97	23.5	513	2	T09739	aspartic endopepti
26	96.5	23.4	101	1	S49145	amoebapore C precu
27	95	23.1	79	1	LNPG1	pulmohary surfacta
28	95	23.1	369	2	I46531	surfactant protein
29	92	22.3	509	2	S49349	cyprosin (EC 3.4.2
30	91	22.1	370	1	LNRBB	pulmonary surfacta
31	91	22.1	381	1	LNHUB	pulmonary surfacta
32	91	22.1	508	2	D85056	probable aspartic
33	90.5	22.0	96	1	S49144	amoebapore B precu
34	90.5	22.0	98	1	S25283	amoebapore A precu
35	89.5	21.7	205	2	B89567	protein T08A9.7 [i
36	89	21.6	314	2	T15674	hypothetical prote
37	87	21.1	195	2	T15676	hypothetical prote
38	84.5	20.5	129	2	S55044	NK-lysin protein -
39	82.5	20.0	280	2	PC4080	aspartic proteinas
40	81.5	19.8	223	2	E89567	protein T08A9.9 [i
41	79	19.2	650	2	T00617	endostyle-specific
42	78.5	19.1	74	2	C89567	protein T08A9.10 [
43	78	18.9	506	2	S71591	aspartic proteinas
44	77.5	18.8	572	2	T27869	sphingomyelin phos
45	76	18.4	306	2	T09915	hypothetical prote

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OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:37 ; Search time 23.4437 Seconds  
 (without alignments)  
 3156.550 Million cell updates/sec

Title: US-10-801-517-2  
 Perfect score: 412  
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPVELVCSMLHLC 80

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	412	100.0	452	2	Q5R406_PONPY	Q5r406 pongo pygma
2	412	100.0	524	1	SAP_HUMAN	P07602 h proactiva
3	412	100.0	524	2	Q53FJ5_HUMAN	Q53fj5 homo sapien
4	412	100.0	524	2	Q5JQ36_HUMAN	Q5jq36 homo sapien
5	412	100.0	527	2	Q5NVD5_PONPY	Q5nvd5 pongo pygma
6	412	100.0	530	2	Q59EN5_HUMAN	Q59en5 homo sapien
7	412	100.0	559	2	Q5JQ37_HUMAN	Q5jq37 homo sapien
8	405	98.3	526	2	Q5R4U7_PONPY	Q5r4u7 pongo pygma
9	397	96.4	497	2	Q4R590_MACFA	Q4r590 m brain cdn
10	346	84.0	525	1	SAP_BOVIN	P26779 b proactiva
11	261	63.3	81	1	SAP_CAVPO	P20097 cavia porce
12	210	51.0	512	2	Q7SY70_XENLA	Q7sy70 xenopus lae
13	207	50.2	550	2	Q4RQ38_TETNG	Q4rq38 tetraodon n
14	205	49.8	520	2	Q6P3G7_BRARE	Q6p3g7 brachydanio
15	205	49.8	520	2	Q6PH48_BRARE	Q6ph48 brachydanio
16	205	49.8	520	2	Q8UVZ4_BRARE	Q8uvz4 brachydanio
17	205	49.8	522	2	Q9DG82_BRARE	Q9dg82 brachydanio
18	203	49.3	518	1	SAP_CHICK	O13035 gallus gall
19	193	46.8	518	2	Q642S6_XENLA	Q642s6 xenopus lae
20	193	46.8	553	2	Q6P7A4_RAT	Q6p7a4 rattus norv
21	193	46.8	554	1	SAP_RAT	P10960 rattus norv
22	174	42.2	554	2	Q3TKB2_MOUSE	Q3tcb2 mus musculu
23	174	42.2	554	2	Q3TKK3_MOUSE	Q3tck3 mus musculu
24	171	41.5	200	2	Q75K05_DICDI	Q75k05 dictyosteli

25	169	41.0	527	2	Q3TWM9_MOUSE	Q3twm9 mus musculu
26	169	41.0	545	2	Q3UAS4_MOUSE	Q3uas4 m bone marr
27	169	41.0	551	2	Q3UE29_MOUSE	Q3ue29 mus musculu
28	169	41.0	553	2	Q3TXJ0_MOUSE	Q3txj0 m osteoclas
29	169	41.0	554	2	Q3TID4_MOUSE	Q3tid4 mus musculu
30	169	41.0	554	2	Q3TIT5_MOUSE	Q3tit5 mus musculu
31	169	41.0	554	2	Q3TWE9_MOUSE	Q3twe9 mus musculu
32	169	41.0	554	2	Q3TWF9_MOUSE	Q3twf9 mus musculu
33	169	41.0	554	2	Q3TXP9_MOUSE	Q3txp9 mus musculu
34	169	41.0	554	2	Q3U5W2_MOUSE	Q3u5w2 mus musculu
35	169	41.0	554	2	Q3U825_MOUSE	Q3u825 mus musculu
36	169	41.0	554	2	Q3U897_MOUSE	Q3u897 mus musculu
37	169	41.0	554	2	Q3U8C4_MOUSE	Q3u8c4 mus musculu
38	169	41.0	554	2	Q8BFQ1_MOUSE	Q8bfq1 m 2 days ne
39	169	41.0	557	1	SAP_MOUSE	Q61207 mus musculu
40	169	41.0	557	2	Q3UFE8_MOUSE	Q3ufe8 mus musculu
41	166	40.3	554	2	Q3TWL8_MOUSE	Q3twl8 mus musculu
42	164	39.8	522	2	Q54Q68_DICDI	Q54q68 dictyosteli
43	163	39.6	336	2	Q54LG3_DICDI	Q54lg3 dictyosteli
44	158	38.3	965	2	O15997_BOMMO	O15997 bombyx mori
45	155	37.6	245	2	Q5ZL62_CHICK	Q5zl62 gallus gall